Sequence Search Lummary

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

August 12, 2003, 08:37:17; Search time 6073 Seconds

(without alignments)

11283.324 Million cell updates/sec

Title:

US-09-938-641-1

Perfect score:

1675

Sequence:

1 gccaaccqcagggcatttac.....ttactggcagcacgatgatc 1675

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched:

2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters:

5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

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- 2: gb htg:*
- 3: gb in:* 4: gb om:*
- 5: gb ov:*
- 6: gb pat:*
- 7: gb_ph:*
- 8: gb pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb vi:*
- 15: em ba:*
- 16: em fun:*
- 17: em hum:*
- 18: em in:*
- 19: em_mu:*
- 20: em om:*
- 21: em or:*
- 22: em ov:* 23: em pat:*
- 24: em_ph:*
- 25: em_pl:* 26: em ro:*
- 27: em sts:*

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37: em_htg_vrt:*
38: em_sy:*
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40: em_htgo_mus:*
41: em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ult No.	Score	Query Match	Length	DB	ID	Description
	. 1	1675	100.0	1675	6	AX394436 Appl's Wo	AX394436 Sequence
	2	1675	100.0	337200	1	APOUS 280 NAFAGENA	AP005280 Corvnebac
	3	1675	100.0	349980	6	AX127149 * EP 1108770	AX127149 Sequence -Seg 7065
	4	981	58.6	981	6	AX122198	AX122198 Sequence
	5	981	58.6	981	6	BD164315	BD164315 Novel pol
	6	781.2	46.6	303250	1	AP005220	AP005220 Corynebac
	7	357	21.3	2550	6	AX122197	AX122197 Sequence
	8	357	21.3	2550	6	BD164314	BD164314 Novel pol
	9	235.8	14.1	1665	1	MAU18263 .	U18263 Mycobacteri
	10	220.8	13.2	311000	1	SCO939122	AL939122 Streptomy
	11	217.2	13.0	3014	1	AF186371	AF186371 Streptomy
	12	207.2	12.4	1901	1	AF034861	AF034861 Mycobacte
С	13	202	12.1	302300	1	AP005034	AP005034 Streptomy
	14	195.8	11.7	1365	1	AF127219	AF127219 Streptomy
С	15	180.4	10.8	342300	1	MLEPRTN8	AL583924 Mycobacte
С	16	173.2	10.3	37114	1		L01095 M. leprae g
	17	167.6	10.0	710	1	MXU43810	U43810 Mycobacteri
	18	160	9.6	788	1		U43811 Mycobacteri
	19	135.2	8.1	13075		AE004946	AE004946 Pseudomon.
С	20	131.6	7.9	11418	1	AE012182	AE012182 Xanthomon
	21	129		142665	1		AE016794 Pseudomon
С	22	126.4		203050	1		AL646071 Ralstonia
С	23	122.8	7.3	3300		ECU74302	U74302 Erwinia car
С	24	121.6	7.3	11376	1	AE011722	AE011722 Xanthomon
	25	121.4	7.2	4027	1	XCU94336	U94336 Xanthomonas
	26	121.4	7.2	4044	1	AF315582	AF315582 Pseudomon
С	-27	117.4	7.0	10951	1	AE006027	AE006027 Caulobact
С	28	116.4		313518	1		AE016856 Pseudomon
	29	113.2	6.8	4910	1		AY040244 Burkholde
	30	106.6	6.4	1900	6		A00047 E.coli mor
	31	106	6.3	1179	1		X52666 E.coli oxyR
	32	106	6.3	1264	1		J04553 E.coli oxyR
	33	106	6.3	1471	1	ECOXYR	X16531 Escherichia

OM nucleic - nucleic search, using sw model

Run on: August 12, 2003, 08:12:07; Search time 470 Seconds

(without alignments)

9620.338 Million cell updates/sec

Title: US-09-938-641-1

Perfect score: 1675

Sequence: 1 gccaaccgcagggcatttac.....ttactggcagcacgatgatc 1675

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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25: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result				8				
1	Re	sult		Query				
3 981 58.6 981 22 AAR680530 Jakagua & F. Worklood Glutamicum codin 4 981 58.6 981 22 AAR67079 C glutamicum codin 5 357 21.3 2550 22 AAR67078 C glutamicum codin 6 357 21.3 2550 25 ACA00582 C. glutamicum cedin 7 177 10.6 177 25 ACA00582 C. glutamicum deri 8 106 6.3 1900 10 AAN91492 Escherichia colin 8 106 6.3 1900 10 AAN91492 Escherichia colin 10 85 5.1 1089 22 AAF28527 Genomic fragment # 10 85 5.1 1089 22 AAF28527 Genomic fragment # 11 85 5.1 1089 22 AAF28527 Genomic fragment # 12 72.4 4.3 9922 23 AAS59594 Propionibacterium 13 72.2 4.3 2058 9 AAN80093 Sequence of BamHI/ 15 69 4.1 886 24 ABR74064 Bacillus lichenifo 16 65.8 3.9 918 25 ABZ41541 N. gonorrhoeae nuc 17 65.8 3.9 918 25 ABZ41541 N. gonorrhoeae nuc 18 65.2 3.9 1050 24 ABL56492 Nucleotide sequenc 19 65.2 3.9 349980 22 AAR68533 C glutamicum codin 20 65.2 3.9 349980 22 AAR68533 C glutamicum codin 21 65 3.9 344 21 AAC74498 Human ORFX ORFS 9 24 64.6 3.9 349980 21 AAR81400 N. meningitidis pa 24 64.6 3.9 349980 21 AAR81400 N. meningitidis pa 24 64.6 3.9 349980 21 AAR81400 N. meningitidis pa 24 64.6 3.9 349980 21 AAR81400 N. meningitidis pa 25 64.6 3.9 349980 21 AAR81400 N. meningitidis pa 26 64.6 3.9 1437668 21 AAR81490 N. meningitidis B 27 64.4 3.8 837 22 AAF88315 S. spinosa DNA fra 28 64.4 3.8 80161 20 AAZ21501 DNA fragment of Sa 29 64.4 3.8 80161 20 AAZ21501 DNA fragment of Sa 30 64.4 3.8 80161 20 AAZ21501 DNA fragment of Sa 31 62.8 3.7 13020 24 ABQ8883 S. spinosa DNA fra 32 60.2 3.6 349980 22 AAF88315 S. spinosa DNA fra 33 60.2 3.6 3.9 349980 22 AAF88315 S. spinosa DNA fra 34 60.2 3.6 349980 22 AAF88315 S. spinosa DNA fra 35 60.2 3.6 349980 22 AAF88315 S. spinosa DNA fra 36 60.2 3.6 349980 22 AAF88315 S. spinosa DNA fra 37 68.8 3.5 103599 23 ABX04971 S. cinnamonensis m 38 60.2 3.6 349980 22 AAF88315 S. spinosa DNA fra 39 57.8 3.5 103599 23 ABX04971 S. cinnamonensis m 40 57.6 3.4 30400 22 AAH68526 C glutamicum codin 41 57.6 3.4 30400 22 AAH68193 C glutamicum codin 42 56.6 3.4 903		No.	Score	Match	Length	DB	ID	Description
3 981 58.6 981 22 AAR680530 Jakagua & F. Worklood Glutamicum codin 4 981 58.6 981 22 AAR67079 C glutamicum codin 5 357 21.3 2550 22 AAR67078 C glutamicum codin 6 357 21.3 2550 25 ACA00582 C. glutamicum cedin 7 177 10.6 177 25 ACA00582 C. glutamicum deri 8 106 6.3 1900 10 AAN91492 Escherichia colin 8 106 6.3 1900 10 AAN91492 Escherichia colin 10 85 5.1 1089 22 AAF28527 Genomic fragment # 10 85 5.1 1089 22 AAF28527 Genomic fragment # 11 85 5.1 1089 22 AAF28527 Genomic fragment # 12 72.4 4.3 9922 23 AAS59594 Propionibacterium 13 72.2 4.3 2058 9 AAN80093 Sequence of BamHI/ 15 69 4.1 886 24 ABR74064 Bacillus lichenifo 16 65.8 3.9 918 25 ABZ41541 N. gonorrhoeae nuc 17 65.8 3.9 918 25 ABZ41541 N. gonorrhoeae nuc 18 65.2 3.9 1050 24 ABL56492 Nucleotide sequenc 19 65.2 3.9 349980 22 AAR68533 C glutamicum codin 20 65.2 3.9 349980 22 AAR68533 C glutamicum codin 21 65 3.9 344 21 AAC74498 Human ORFX ORFS 9 24 64.6 3.9 349980 21 AAR81400 N. meningitidis pa 24 64.6 3.9 349980 21 AAR81400 N. meningitidis pa 24 64.6 3.9 349980 21 AAR81400 N. meningitidis pa 24 64.6 3.9 349980 21 AAR81400 N. meningitidis pa 25 64.6 3.9 349980 21 AAR81400 N. meningitidis pa 26 64.6 3.9 1437668 21 AAR81490 N. meningitidis B 27 64.4 3.8 837 22 AAF88315 S. spinosa DNA fra 28 64.4 3.8 80161 20 AAZ21501 DNA fragment of Sa 29 64.4 3.8 80161 20 AAZ21501 DNA fragment of Sa 30 64.4 3.8 80161 20 AAZ21501 DNA fragment of Sa 31 62.8 3.7 13020 24 ABQ8883 S. spinosa DNA fra 32 60.2 3.6 349980 22 AAF88315 S. spinosa DNA fra 33 60.2 3.6 3.9 349980 22 AAF88315 S. spinosa DNA fra 34 60.2 3.6 349980 22 AAF88315 S. spinosa DNA fra 35 60.2 3.6 349980 22 AAF88315 S. spinosa DNA fra 36 60.2 3.6 349980 22 AAF88315 S. spinosa DNA fra 37 68.8 3.5 103599 23 ABX04971 S. cinnamonensis m 38 60.2 3.6 349980 22 AAF88315 S. spinosa DNA fra 39 57.8 3.5 103599 23 ABX04971 S. cinnamonensis m 40 57.6 3.4 30400 22 AAH68526 C glutamicum codin 41 57.6 3.4 30400 22 AAH68193 C glutamicum codin 42 56.6 3.4 903	_	 1	1675	100.0	1675	24	ABT.56944	And's DE Corynphagtorium Ov
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8 106 6.3 1900 10 AAN91492 Escherichia coli m c 9 87.4 5.2 19619 22 AAF28527 Genomic fragment # C 10 85 5.1 1089 22 AAF67080 C glutamicum codin c 11 85 5.1 1089 25 ACA00586 C. glutamicum deri c 12 72.4 4.3 9922 23 AAS59594 Propionibacterium c 12 72.4 4.3 9922 23 AAS59594 Propionibacterium c 14 72.2 4.3 2058 P AAN80093 Sequence of BamHI/c 15 69 4.1 886 24 ABK74064 Bacillus lichenifo c 16 65.8 3.9 918 25 AB241010 N. gonorrhoeae nuc 17 65.8 3.9 918 25 AB241010 N. gonorrhoeae nuc 18 65.2 3.9 705 22 AAH67844 C glutamicum codin c 19 65.2 3.9 1050 24 AB67844 C glutamicum codin c 21 65 3.9 34980 22 AAH68533 C glutamicum codin c 21 65 3.9 344 21 AAC74498 Human ORFX ORF53 p 2 24 64.6 3.9 19231 21 AAA81470 N. meningitidis pa 24 64.6 3.9 349980 21 AAF21544 Neisseria meningit 25 64.6 3.9 349980 21 AAF21544 Neisseria meningit 25 64.6 3.9 349980 21 AAF2154 Neisseria meningit 25 64.6 3.9 349980 22 AAF88312 S. spinosa DNA fra 28 64.4 3.8 85624 22 AAF88315 S. spinosa DNA fra 28 64.4 3.8 85624 22 AAF88315 S. spinosa DNA fra 28 64.4 3.8 85624 22 AAF88315 S. spinosa DNA fra 28 64.4 3.8 8510 20 AAZ21501 DNA fragment of Sa 36 60.2 3.6 349980 22 AAH68525 C glutamicum codin 27 64.4 3.8 80161 20 AAZ21501 DNA fragment of Sa 59.2 3.5 1830121 17 AAT42063 B. lactofermentum codin 37 58.8 3.5 1830121 17 AAT42063 B. lactofermentum codin 37 58.8 3.5 1830121 17 AAT42063 B. lactofermentum codin 37 58.8 3.5 1830121 17 AAT42063 B. lactofermentum codin 37 58.8 3.5 1830121 17 AAT42063 B. lactofermentum codin 44 56.6 3.4 924 22 AAH68524 C glutamicum codin 45 66.6 3.4 924 22 AAH68524 C glutamicum codin 45 66.6 3.4 924 22 AAH68534 C glutamicum codin 45 66.6 3.4 924 22 AAH68534 C glutamicum codin 45 66.6 3.4 924 22 AAH68534 C glutamicum codin 45 66.6 3.4 924 22 AAH68534 C glutamicum codin 45 66.6 3.4 924 22 AAH68534 C glutamicum codin 45 66.6 3.4 924 22 AAH68534 C glutamicum codin 45 66.6 3.4 924 22 AAH68534 C glutamicum codin 45 66.6 3.4 924 22 AAH68534 C glutamicum codin 45 66.6 3.4 924 22 AAH68534 C glutamicum codin 45 66.6 3.4 924 22 AAH68534 C glut	С							
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25 64.6 3.9 349980 24 ABQ81842 Bifidobacterium 10 26 64.6 3.9 1437668 21 AAA81490 N. meningitidis B 27 64.4 3.8 837 22 AAF88334 S. spinosa DNA fra 28 64.4 3.8 45624 22 AAF88315 S. spinosa DNA fra C 29 64.4 3.8 50000 22 AAF88312 S. spinosa DNA fra C 30 64.4 3.8 80161 20 AAZ21501 DNA fragment of Sa C 31 62.8 3.7 13020 24 ABQ78873 S. roseosporus dap 32 60.2 3.6 909 22 AAH65641 C. glutamicum codin 33 60.2 3.6 1311 24 ABA95150 C. glutamicum lysk 34 60.2 3.6 349980 22 AAH68525 C. glutamicum codin 35 60.2 3.6 349980 22 AAH68525 C. glutamicum codin 36 59.2 3.5 2703 23 AAS92835 DNA encoding novel 37 58.8 3.5 3390 22 AAF26986 B. lactofermentum 40 57.6 3.4 1364 24 ABA91926 Corynebacterium gl C 41 57.6 3.4 309400 22 AAH68534 C. glutamicum codin 36 56.2 3.4 903 25 ACA01299 C. glutamicum codin 36.2 3.4 903 25 ACA01299 C. glutamicum codin 37 56.2 3.4 903 25 ACA01299 C. glutamicum codin 38 56.2 3.4 903 25 ACA01299 C. glutamicum codin 36.2 3.4 903 25 ACA01299 C. glutam		24						
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27 64.4 3.8 837 22 AAF88334 S. spinosa DNA fra 28 64.4 3.8 45624 22 AAF88315 S. spinosa DNA fra C 29 64.4 3.8 50000 22 AAF88312 S. spinosa DNA fra C 30 64.4 3.8 80161 20 AAZ21501 DNA fragment of Sa C 31 62.8 3.7 13020 24 ABQ78873 S. roseosporus dap 32 60.2 3.6 909 22 AAH65641 C. glutamicum codin 33 60.2 3.6 1311 24 ABA95150 C. glutamicum lysk 34 60.2 3.6 349980 22 AAH68525 C. glutamicum codin 35 60.2 3.6 349980 22 AAH68526 C. glutamicum codin 36 59.2 3.5 2703 23 AAS92835 DNA encoding novel 37 58.8 3.5 3390 22 AAF26986 B. lactofermentum 40 57.6 3.4 1364 24 ABA91926 Corynebacterium gl C 41 57.6 3.4 309400 22 AAH68534 C. glutamicum codin 42 56.6 3.4 924 22 AAH68193 C. glutamicum codin 43 56.2 3.4 903 25 ACA01299 C. glutamicum deri 44 55.6 3.3 879 22 AAH65474 C. glutamicum codin		26						
28 64.4 3.8 45624 22 AAF88315 S. spinosa DNA fra C 29 64.4 3.8 50000 22 AAF88312 S. spinosa DNA fra C 30 64.4 3.8 80161 20 AAZ21501 DNA fragment of Sa C 31 62.8 3.7 13020 24 ABQ78873 S. roseosporus dap 32 60.2 3.6 909 22 AAH65641 C. glutamicum codin 33 60.2 3.6 1311 24 ABA95150 C. glutamicum lysk 34 60.2 3.6 349980 22 AAH68525 C. glutamicum codin 35 60.2 3.6 349980 22 AAH68526 C. glutamicum codin 36 59.2 3.5 2703 23 AAS92835 DNA encoding novel 37 58.8 3.5 3390 22 AAF26986 B. lactofermentum C 38 58.2 3.5 1830121 17 AAT42063 Haemophilus influe 39 57.8 3.5 103599 23 ABX04971 S. cinnamonensis m 40 57.6 3.4 1364 24 ABA91926 Corynebacterium gl C 41 57.6 3.4 309400 22 AAH68534 C. glutamicum codin 42 56.6 3.4 924 22 AAH68193 C. glutamicum deri 43 56.2 3.4 903 25 ACA01299 C. glutamicum deri 44 55.6 3.3 879 22 AAH65474 C. glutamicum codin		27	64.4	3.8				· • • • • • • • • • • • • • • • • • • •
C 29 64.4 3.8 50000 22 AAF88312 S. spinosa DNA fra C 30 64.4 3.8 80161 20 AAZ21501 DNA fragment of Sa C 31 62.8 3.7 13020 24 ABQ78873 S. roseosporus dap 32 60.2 3.6 909 22 AAH65641 C glutamicum codin 33 60.2 3.6 1311 24 ABA95150 C. glutamicum codin 34 60.2 3.6 349980 22 AAH68525 C glutamicum codin 35 60.2 3.6 349980 22 AAH68526 C glutamicum codin 36 59.2 3.5 2703 23 AAS92835 DNA encoding novel 37 58.8 3.5 3390 22 AAF26986 B. lactofermentum 40 57.8 3.5 103599 23 ABX04971 S. cinnamonensis m 40 57.6 3.4 309400 22		28						
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33 60.2 3.6 1311 24 ABA95150 C. glutamicum lysR 34 60.2 3.6 349980 22 AAH68525 C glutamicum codin 35 60.2 3.6 349980 22 AAH68526 C glutamicum codin 36 59.2 3.5 2703 23 AAS92835 DNA encoding novel 37 58.8 3.5 3390 22 AAF26986 B. lactofermentum 6 38 58.2 3.5 1830121 17 AAT42063 Haemophilus influe 39 57.8 3.5 103599 23 ABX04971 S. cinnamonensis m 40 57.6 3.4 1364 24 ABA91926 Corynebacterium gl 6 C 41 57.6 3.4 309400 22 AAH68534 C glutamicum codin 42 56.6 3.4 924 22 AAH68193 C glutamicum codin 43 56.2 3.4 903 25 ACA01299 C. glutamicum deri 44 55.6 3.3 879 22 AAH65474 C glutamicum codin		32	60.2	3.6		22		
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35 60.2 3.6 349980 22 AAH68526 C glutamicum codin 36 59.2 3.5 2703 23 AAS92835 DNA encoding novel 37 58.8 3.5 3390 22 AAF26986 B. lactofermentum 6 38 58.2 3.5 1830121 17 AAT42063 Haemophilus influe 39 57.8 3.5 103599 23 ABX04971 S. cinnamonensis m 40 57.6 3.4 1364 24 ABA91926 Corynebacterium gl 6 C 41 57.6 3.4 309400 22 AAH68534 C glutamicum codin 42 56.6 3.4 924 22 AAH68193 C glutamicum codin 43 56.2 3.4 903 25 ACA01299 C. glutamicum deri 44 55.6 3.3 879 22 AAH65474 C glutamicum codin		34	60.2	3.6	349980	22		
36 59.2 3.5 2703 23 AAS92835 DNA encoding novel 37 58.8 3.5 3390 22 AAF26986 B. lactofermentum 6 38 58.2 3.5 1830121 17 AAT42063 Haemophilus influe 39 57.8 3.5 103599 23 ABX04971 S. cinnamonensis m 40 57.6 3.4 1364 24 ABA91926 Corynebacterium gl 6 41 57.6 3.4 309400 22 AAH68534 C glutamicum codin 42 56.6 3.4 924 22 AAH68193 C glutamicum codin 43 56.2 3.4 903 25 ACA01299 C. glutamicum deri 44 55.6 3.3 879 22 AAH65474 C glutamicum codin		35	60.2	3.6	349980	22		
37 58.8 3.5 3390 22 AAF26986 B. lactofermentum C 38 58.2 3.5 1830121 17 AAT42063 Haemophilus influe 39 57.8 3.5 103599 23 ABX04971 S. cinnamonensis m 40 57.6 3.4 1364 24 ABA91926 Corynebacterium gl C 41 57.6 3.4 309400 22 AAH68534 C glutamicum codin 42 56.6 3.4 924 22 AAH68193 C glutamicum codin 43 56.2 3.4 903 25 ACA01299 C. glutamicum deri 44 55.6 3.3 879 22 AAH65474 C glutamicum codin		36	59.2	3.5	2703	23		
C 38 58.2 3.5 1830121 17 AAT42063 Haemophilus influe 39 57.8 3.5 103599 23 ABX04971 S. cinnamonensis m 40 57.6 3.4 1364 24 ABA91926 Corynebacterium gl C 41 57.6 3.4 309400 22 AAH68534 C glutamicum codin 42 56.6 3.4 924 22 AAH68193 C glutamicum codin 43 56.2 3.4 903 25 ACA01299 C. glutamicum deri 44 55.6 3.3 879 22 AAH65474 C glutamicum codin		37	58.8	3.5	3390	22		
39 57.8 3.5 103599 23 ABX04971 S. cinnamonensis m 40 57.6 3.4 1364 24 ABA91926 Corynebacterium gl c 41 57.6 3.4 309400 22 AAH68534 C glutamicum codin 42 56.6 3.4 924 22 AAH68193 C glutamicum codin 43 56.2 3.4 903 25 ACA01299 C. glutamicum deri 44 55.6 3.3 879 22 AAH65474 C glutamicum codin	С	38	58.2	3.5	1830121	17		
40 57.6 3.4 1364 24 ABA91926 Corynebacterium gl c 41 57.6 3.4 309400 22 AAH68534 C glutamicum codin 42 56.6 3.4 924 22 AAH68193 C glutamicum codin 43 56.2 3.4 903 25 ACA01299 C. glutamicum deri 44 55.6 3.3 879 22 AAH65474 C glutamicum codin		39	57.8	3.5	103599	23	ABX04971	
C 41 57.6 3.4 309400 22 AAH68534 C glutamicum codin 42 56.6 3.4 924 22 AAH68193 C glutamicum codin 43 56.2 3.4 903 25 ACA01299 C. glutamicum deri 44 55.6 3.3 879 22 AAH65474 C glutamicum codin		40	57.6	3.4				
42 56.6 3.4 924 22 AAH68193 C glutamicum codin 43 56.2 3.4 903 25 ACA01299 C. glutamicum deri 44 55.6 3.3 879 22 AAH65474 C glutamicum codin	С	41	57.6	3.4	309400			-
43 56.2 3.4 903 25 ACA01299 C. glutamicum deri 44 55.6 3.3 879 22 AAH65474 C glutamicum codin		42		3.4	924	22		
44 55.6 3.3 879 22 AAH65474 C glutamicum codin		43		3.4	903	25		
			55.6	3.3	879	22		
		45	55.6	3.3	879	25	ACA02151	

OM nucleic - nucleic search, using sw model

Run on: August 12, 2003, 11:04:33; Search time 392 Seconds

(without alignments)

9361.817 Million cell updates/sec

Title: US-09-938-641-1

Perfect score: 1675

Sequence: 1 gccaaccgcagggcatttac.....ttactggcagcacgatgatc 1675

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1487832 segs, 1095472286 residues

Total number of hits satisfying chosen parameters: 2975664

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2 6/ptodata/1/pubpna/US07 PUBCOMB.seq:*

2: /cgn2 6/ptodata/1/pubpna/PCT NEW PUB.seg:*

3: /cgn2 6/ptodata/1/pubpna/US06 NEW PUB.seg:*

/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

/cgn2_6/ptodata/1/pubpna/US07_NEW PUB.seq:*

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7: /cgn2 6/ptodata/1/pubpna/US08 NEW PUB.seg:*

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9: /cgn2_6/ptodata/1/pubpna/US09A PUBCOMB.seg:*

10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2 6/ptodata/1/pubpna/US09C PUBCOMB.seq:*

12: /cgn2 6/ptodata/1/pubpna/US09 NEW PUB.seg:*

13: /cgn2 6/ptodata/1/pubpna/US10A PUBCOMB.seq:*

14: /cgn2 6/ptodata/1/pubpna/US10B PUBCOMB.seq:*

15: /cgn2 6/ptodata/1/pubpna/US10 NEW PUB.seq:* /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:* 16:

17: /cgn2 6/ptodata/1/pubpna/US60 PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

US 20020197605-A1

			8				
Res	ult		Query				1
	No.	Score	Match	Length I	OB	ID	Descr#ption
	1	1675	100.0	1675	9	US-09-938-641-1 instant	Seguence 1, Appli
	2	1675		3309400	10		
	3	981	58.6	981	10	US-09-738-626-2114	Sequence 2114, Ap
	4	357	21.3	2550	10	US-09-738-626-2113	Sequence 2113, Ap
	5	202	12.1	1008	14	US-10-156-761-3218	Sequence 3218, Ap
С	6	202		9025608	14		Sequence 1, Appli
	7	106.4	6.4	951	14	US-10-156-761-3347	Sequence 3347, Ap
	8	86.6	5.2	891	14	US-10-156-761-7285	Sequence 7285, Ap
С	9	85	5.1	1089	10	US-09-738-626-2115	Sequence 2115, Ap
	10	81	4.8	936	14	US-10-156-761-4774	Sequence 4774, Ap
	11	69	4.1	886	10	US-09-974-300-1355	Sequence 1355, Ap
	12	65.2	3.9	705	10	US-09-738-626-2879	Sequence 2879, Ap
С	13	65.2	3.9	3309400	10	US-09-738-626-1	Sequence 1, Appli
	14	65	3.9	987	14	US-10-156-761-2141	Sequence 2141, Ap
	15	62.8	3.7	912	14	US-10-156-761-1515	Sequence 1515, Ap
	16	62.8	3.7	9025608	14	US-10-156-761-1	Sequence 1, Appli
	17	60.2	3.6	888	14	US-10-156-761-7214	Sequence 7214, Ap
	18	60.2	3.6	909	10	US-09-738-626-676	Sequence 676, App
	19	58.8	3.5	3390	10	US-09-767-878-1	Sequence 1, Appli
C	20	58.2	3.5	1830121	14	US-10-329-960-1	Sequence 1, Appli
	21	58	3.5	2658	14	US-10-156-761-1562	Sequence 1562, Ap
	22	57.6	3.4	1364	9	US-09-826-909-1	Sequence 1, Appli
	23	57.2	3.4	876	14	US-10-156-761-1152	Sequence 1152, Ap
	24	56.6	3.4	924	10	US-09-738-626-3228	Sequence 3228, Ap
	25	56.4	3.4	963	14	US-10-156-761-5097	Sequence 5097, Ap
	26	56	3.3	924	14	US-10-156-761-5287	Sequence 5287, Ap
	27	55.6	3.3	879	10	US-09-738-626-509	Sequence 509, App
С	28	53.2	3.2	6133	14	US-10-114-170-15	Sequence 15, Appl
	29	52.4	3.1	465	10	US-09-974-300-5814	Sequence 5814, Ap
	30	52.2	3.1	602	10	US-09-974-300-5894	Sequence 5894, Ap
	31	51	3.0	912	14	US-10-156-761-761	Sequence 761, App
	32	50	3.0	909	14	US-10-156-761-1341	Sequence 1341, Ap
	33	49.8	3.0	894	14	US-10-156-761-4980	Sequence 4980, Ap
	34	49.2	2.9	903	14	US-10-156 - 761-1615	Sequence 1615, Ap
	35	48.8	2.9	948	14	US-10-156-761-4907	Sequence 4907, Ap
С	36	48.6	2.9	33719	15	US-10-080-170-651	Sequence 651, App
	37	48.2	2.9	918	14	US-10-156-761-6700	Sequence 6700, Ap
	38	48	2.9	520	14	US-10-184-644-332	Sequence 332, App
	39	48	2.9	520	14	US-10-184-634-332	Sequence 332, App
С	40	47.6	2.8	520	14	US-10-184-644-332	Sequence 332, App
С	41	47.6	2.8	520	14	US-10-184-634-332	Sequence 332, App
	42	46.4	2.8	897	14	US-10-156-761-6980	Sequence 6980, Ap
С	43	45.8	2.7	390	9	US-09-790-399-7	Sequence 7, Appli
	44	45.2	2.7	570	14	US-10-156-761-1030	Sequence 1030, Ap
	45	44.6	2.7	868	10	US-09-974-300-1338	Sequence 1338, Ap

ALIGNMENTS

OM nucleic - nucleic search, using sw model

Run on: August 12, 2003, 09:10:43; Search time 3283 Seconds

(without alignments)

12400.243 Million cell updates/sec

Title: US-09-938-641-1

Perfect score: 1675

Sequence: 1 gccaaccgcagggcatttac.....ttactggcagcacgatgatc 1675

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 segs, 12152238056 residues.

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: em estba:*

2: em esthum:*

3: em estin:*

4: em estmu:*

5: em_estov:*

6: em estpl:*

7: em estro:*

em htc:*

9: gb est1:*

10: gb_est2:*

11: gb htc:*

12: gb est3:*

13: gb est4:*

14: gb est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:* 18: em_gss inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em gss rod:*

26: em gss phg:*

27: em_gss_vrl:*

28: gb_gss1:* 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

						SUMMARI	IES
			ક્ર				•
Res	ult		Query				
	No.	Score	Match	Length	DB	ID	Description
	1	87.2	5.2	557	28	BH015055	BH015055 TDGBU22TH
	2	84.8	5.1	989	29	CNS01L69	AL149234 Anopheles
	3	82.8	4.9	581	10	BG456831	BG456831 NF098B09P
	4	82.2	4.9	503	10	BE323006	BE323006 NF011C03P
	5	80.6	4.8	863	29	CNS01JCX	AL146882 Anopheles
	6	77.8	4.6	770	29	CNS01HMH	AL144618 Anopheles
	7	74.8	4.5	793	29	CNS01QXX	AL156709 Anopheles
С	8	74	4.4	984	29	BZ702112	BZ702112 PUBMK94TD
	9	70.2	4.2	890	29	BZ560396	BZ560396 pacs2-164
	10	67.8	4.0	1513	29	BZ568940	BZ568940 pacs2-164
	11	66	3.9	1280	29	BZ578104	BZ578104 msh2 5716
	12	64.4	3.8	394	28	AZ049643	AZ049643 GSSBru013
	13	63.6	3.8	1056	29	BZ558383	BZ558383 pacs1-60_
С	14	59.6	3.6	629	28	AQ991551	AQ991551 Rfc02534
	15	58.6	3.5	829	29	BZ564143	BZ564143 pacs2-164
С	16	56.4	3.4	719	29	BZ562021	BZ562021 pacs2-164
_	17	54.8	3.3	734	28	AY080301	AY080301 AY080301
٠	18	54.4	3.2	1201	13	BX381961	BX381961 BX381961
	19	54.2	3.2	861	29	BZ572433	BZ572433 msh2 2632
С	20	53.8	3.2	780	29	BZ560257	BZ560257 pacs2-164
•	21	53.6	3.2	451	29	BZ422864	BZ422864 id59d05.b
С	22	53.6	3.2	550	29	BZ422004	
C	23	53.2	3.2	721	29	BZ562255	BZ424306 id59d05.g
	24	53.2	3.2	817	29	BZ562233	BZ562255 pacs2-164
	25	53.2	3.2	887	29	BZ577325	BZ566287 pacs2-164
	26	53.2	3.2	590	28		BZ577325 msh2_5355
С	27	53	3.2	787	28	AZ934607	AZ934607 BJBa000
С	28	52.4	3.1	648		AZ934759	AZ934759 BJ_Ba000
	. 29	52.4	3.1	674	9	AA606945	AA606945 vm93e11.r
	30				14	CA403566	CA403566 EL01N0503
C		52.4	3.1	1175	29	BZ568637	BZ568637 pacs2-164
С	31	51.8	3.1	924	29	CC136342	CC136342 NDL.65B10
_	32	51	3.0	897	29	BZ572451	BZ572451 msh2_2640
С	33	49.6	3.0	872	29	BZ551630	BZ551630 pacs1-60_
	34	49.4	2.9	688	28	B07706	B07706 318P1A04311
С	35	49.4	2.9	1161	29	BZ556936	BZ556936 pacs1-60_
	36	49.2	2.9	920	29	BZ569987	BZ569987 msh2_1113
	37	49	2.9	720	28	вн370673	BH370673 AG-ND-140
	38	49	2.9	844	29	BZ574523	BZ574523 msh2_3710
	39	48.8	2.9	473	14	CD212636	CD212636 HS1 $\overline{6}$ CO1
	40	48.8	2.9	1344	29	BZ568929	BZ568929 pacs2-164
С	41	48.6	2.9	610	28	AZ935198	AZ935198 BJBa000
С	42	48.6	2.9	617	12	BI643687	BI643687 EM1_19_B0
С	43	48.6	2.9	783	28	AZ935171	AZ935171 BJBa000
	44	48.2	2.9	836	14	CB853302	CB853302 UI-CF-FN0
	45	47.8	2.9	278	28	AZ302981	AZ302981 GSSBru192

OM nucleic - nucleic search, using sw model

Run on: August 12, 2003, 09:14:58; Search time 124 Seconds

(without alignments)

5962.232 Million cell updates/sec

Title: US-09-938-641-1

Perfect score: 1675

Sequence: 1 gccaaccgcagggcatttac.....ttactggcagcacgatgatc 1675

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2 6/ptodata/1/ina/6A COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Res	ult		% Query				
	No.	Score		Length	DB	ID	Description .
	1	180.4	10.8	37030	4	US-08-311-731A-25	Sequence 25, Appl
	2	133.4	8.0	2094	4	US-09-252-991A-7438	Sequence 7438, Ap
	3	133.4	8.0	3012	4	US-09-252-991A-7498	Sequence 7498, Ap
	4	79.6	4.8	1602	4	US-09-252-991A-6382	Sequence 6382, Ap
	5	79.4	4.7	921	4	US-09-252-991A-3438	Sequence 3438, Ap
С	6	79.4	4.7	984	4	US-09-252-991A-3477	Sequence 3477, Ap
	7	79.4	4.7	1263	4	US-09-252-991A-3462	Sequence 3462, Ap
С	8	79	4.7	945	4 ·	US-09-252-991A-6167	Sequence 6167, Ap
	9	77.6	4.6	732	4	US-09-252-991A-6298	Sequence 6298, Ap
С	10	72.6	4.3	1392	4	US-09-252-991A-3486	Sequence 3486, Ap
С	11	72.2	4.3	2058	1	US-08-358-117-1	Sequence 1, Appli

OM nucleic - nucleic search, using sw model

Run on:

August 12, 2003, 13:17:53 ; Search time 6074 Seconds

(without alignments)

11281.466 Million cell updates/sec

Title:

US-09-938-641-1

Perfect score:

1675

Sequence:

1 gccaaccgcagggcatttac.....ttactggcagcacgatgatc 1675

Scoring table!

OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched:

2888711 segs, 20454813386 residues

Word size :

0

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:*

- 1: qb ba:*
- 2: gb htg:*
- 3: gb in:*
- 4: gb om:*
- 5: gb_ov:*
- 6: gb pat:*
- 7: gb ph:* 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb un:*
- 14: gb vi:*
- 15: em ba:*
- 16: em fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em om:*
- 21: em or:*
- 22: em ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em ro:* 27: em sts:*

```
28: em_un:*
29: em vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em sy:*
39: em_htgo_hum:*
40:
    em_htgo_mus:*
41:
    em htgo other:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Res	ult No.	Score	Query Match	Length	DB	ID	Description
	1	1675	100.0	1675	- 6	 AX394436	7V20442C Campage
	2	1675		337200	1	AP005280	AX394436 Sequence
	3	1675		349980	6	AX127149	AP005280 Corynebac
	4	981	58.6	981	6	AX127149 AX122198	AX127149 Sequence
	5	981	58.6	981	6	BD164315	AX122198 Sequence
	6	357	21.3	2550	6	AX122197	BD164315 Novel pol
	7	357	21.3	2550	6	BD164314	AX122197 Sequence
С	8	85	5.1	1089	6	AX122199	BD164314 Novel pol
C	9	85	5.1	1089	6	BD164316	AX122199 Sequence
C	10	23		268984	3	AE001274 Leishmania	BD164316 Novel pol AE001274 Leishmani
С	11	21		238557	2	AC133482	AC133482 Rattus no
C	12	21		240091	2	AC137350	AC137350 Rattus no
С	13	21		263545	2	AC107182	AC107182 Rattus no
C	14	21		303250	1	AP005220	
С	15	20	1.2	20	6	AX394439	AP005220 Corynebac
c	16	20	1.2	183	6	AX121529	AX394439 Sequence
С	17	20	1.2	183	6	BD163646	AX121529 Sequence BD163646 Novel pol
С	18	20	1.2	1285	10	BC046342	BC046342 Mus muscu
· C	19	20	1.2	1294	10	BC0240342 BC024048	
c	20	20	1.2	1387	10	MMU251200	BC024048 Mus muscu AJ251200 Mus muscu
С	21	20	1.2	2434	10	MMU245737	AJ245737 Mus muscu
c	22	20	1.2	5568	4	SSIFNG	X53085 S.scrofa DN
0	23	20	1.2	11982	1	AE008075	AE008075 Agrobacte
	24	20	1.2	12023	1	AE000073	AE009110 Agrobacte
	25	20		152888	9	AC091491	AC091491 Homo sapi
С	26	20		154342	2	70005605	
C	27	20		158169	2	AC141751	AP005695 Oryza sat
С	28	20		162183	2	AP005822	AC141751 Apis mell
C	29	20		162949	9	AC090943	AP005822 Oryza sat
	30	20		181034	2	AC135486	AC090943 Homo sapi AC135486 Rattus no
	31	20		189054	2	AC135272	
	32	20		194985	10	AC002406	AC135272 Rattus no
С	33	20		195636	2	AC139391	AC002406 Mouse chr
C	55	20	1.2	190000	۷	WC103031	AC139391 Rattus no

OM nucleic - nucleic search, using sw model

Run on: August 12, 2003, 11:59:28; Search time 470 Seconds

(without alignments)

9620.338 Million cell updates/sec

Title: US-09-938-641-1

Perfect score:

Sequence: 1 gccaaccgcagggcatttac.....ttactggcagcacgatgatc 1675

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N Geneseq 19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*

/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*

/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*

/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*

7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*

/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*

9: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*

10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*

/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:* 11:

12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*

13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*

/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:* 14:

/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:* 15:

/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:* 16:

17:

/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:* 18:

/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:* 19:

/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:* /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:* 20:

/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:* 21:

22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*

23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*

/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES .

			ક્ર				
Res	sult		Query				
	No.	Score	Match	Length	DB	ID	Description
	1	 1675	100.0	1675	24	ABL56944	· Corynebacterium Ox
	2	1675		349980	22	AAH68530	Colynebacterium ox C glutamicum codin
	3	981	58.6	981	22	AAH67079	. C glutamicum codin
	4	981	58.6	981	25	ACA00583	
	5	357	21.3	2550	22	AAH67,078	C. glutamicum deri
	6	357	21.3	2550	25	ACA00582	C glutamicum codin
С	7	177	10.6	177	25	ACA00582 ACA00584	C. glutamicum deri
С	8	85	5.1	1089	22	AAH67080	C. glutamicum deri
С	9	85	5.1	1089	25	ACA00586	C glutamicum codin
С	10	20	1.2	20	24	ABL56946	C. glutamicum deri
С	11	20	1.2	183	22	AAH66410	Corynebacterium Ox
C	12	20	1.2	204	25	ACA01550	C glutamicum codin
С	13	20	1.2	748	22	AAL24182	C. glutamicum deri
C	14	20		349980	22		Human breast cance
	15	19	1.1	402	24	AAH68528	C glutamicum codin
	16	19	1.1	530	24	ABZ08413	Human leukocyte de
0	17	19			22	ABZ08416	Human leukocyte de
C	18	19	1.1	1263	22	AAH68278	C glutamicum codin
C	19	19	1.1	1386 3926		AAF67922	Corynebacterium gl
_	20		1.1		19	AAV29577	Pythium oligandrum
С	21	19	1.1	3926	19	AAV29577	Pythium oligandrum
_	22	19	1.1	3926	19	AAV29576	Pythium oligandrum
С	23	19	1.1	3926	19	AAV29576	Pythium oligandrum
_	23 24	19	1.1	3933	19	AAV29578	Pythium oligandrum
C	24 25	19	1.1	3933	19	AAV29578	Pythium oligandrum
С	26	19	1.1	44820	24	AAS19703	Reference sequence
	27	19		148567	25	ABS55500	Gene encoding huma
	28	19	1.1	309400	22	AAH68534	C glutamicum codin
		18	1.1	30	24	ABL56945	Corynebacterium Ox
_	29 30	18	1.1	201	25	ABX20985	Human GDP-mannose
С	31	18	1.1	289	24	ABS51630	Human cDNA encodin
C	32	18	1.1	360	22	AAI93049	Human polynucleoti
C C	33	18	1.1	423	21	AAC57932	Arachidonic acid m
C	33 34	18	1.1	423	21	AAC57933	Arachidonic acid m
С	35	18 18	1.1	423	21	AAC57934	Arachidonic acid m
C	36	18	1.1	423	21	AAC57935	Arachidonic acid m
	37		1.1	491	24	ABL87838	Human ovarian canc
	38	18	1.1	578	21	AAF10311	Fusarium venenatum
		18	1.1	723	21	AAC48808	Arabidopsis thalia
^	39 40	18	1.1	723	24	ABZ13849	Arabidopsis thalia
C	40	18	1.1	922	22	AAH34856	Human colon cancer
С	41	18	1.1	922	24	ABL90444	Human polynucleoti
	42	18	1.1	925	21	AAA02110	Human colon cancer
	43 44	18	1.1	1024	21	AAC37755	Arabidopsis thalia
	44	18	1.1	1026	21	AAC48812	Arabidopsis thalia
	40	18	1.1	1049	21	AAC36711	Arabidopsis thalia

OM nucleic - nucleic search, using sw model

Run on: August 12, 2003, 15:20:29; Search time 390 Seconds

(without alignments)

9409.826 Million cell updates/sec

Title: US-09-938-641-1

Perfect score: 1675

Sequence: 1 gccaaccgcagggcatttac.....ttactggcagcacgatgatc 1675

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 1487832 segs, 1095472286 residues

Word size :

Total number of hits satisfying chosen parameters: 2975664

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2 6/ptodata/1/pubpna/US07 PUBCOMB.seg:*

/cgn2 6/ptodata/1/pubpna/PCT NEW PUB.seq:*

3: /cgn2 6/ptodata/1/pubpna/US06 NEW PUB.seg:*

/cgn2 6/ptodata/1/pubpna/US06 PUBCOMB.seq:*

/cgn2_6/ptodata/1/pubpna/US07 NEW PUB.seq:*

/cgn2 6/ptodata/1/pubpna/PCTUS PUBCOMB.seg:*

7: /cgn2 6/ptodata/1/pubpna/US08 NEW PUB.seq:*

/cgn2_6/ptodata/1/pubpna/US08 PUBCOMB.seq:*

9: /cgn2 6/ptodata/1/pubpna/US09A PUBCOMB.seg:*

10: /cgn2 6/ptodata/1/pubpna/US09B PUBCOMB.seq:*

/cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:* 11:

12: /cgn2 6/ptodata/1/pubpna/US09 NEW PUB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

14: /cgn2 6/ptodata/1/pubpna/US10B PUBCOMB.seq:*

15: /cgn2 6/ptodata/1/pubpna/US10 NEW PUB.seg:*

16: /cgn2 6/ptodata/1/pubpna/US60 NEW PUB.seg:*

17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			8				
Res			Query				
	No.	Score	Match	Length I	DВ	ID	Description
	1	1675	100.0	1675	9	US-09-938-641-1	Sequence 1, Appli
	2	1675		3309400	1(Sequence 1, Appli
	3	981	58.6	981	10	US-09-738-626-2114	Sequence 2114, Ap
	4	357	21.3	2550	10	US-09-738-626-2113	Sequence 2113, Ap
С	5	85	5.1	1089	10	US-09-738-626-2115	Sequence 2115, Ap
С	6	20	1.2	20	9	US-09-938-641-4	Sequence 4, Appli
С	7	20	1.2	183	10	US-09-738-626-1445	Sequence 1445, Ap
	8	19	1.1	. 628	13	US-10-027-632-290181	Sequence 290181,
	9	19	1.1	882	13	US-10-027-632-173402	Sequence 173402,
	10	19	1.1	882	13	US-10-027-632-173403	Sequence 173403,
С	11	19	1.1	1263	10	US-09-738-626-3313	Sequence 3313, Ap
	12	19	1.1	1848	14	US-10-156-761-3041	Sequence 3041, Ap
	13	19	1.1	2658	14	US-10-156-761-1562	Sequence 1562, Ap
	14	19	1.1	148567	10	US-09-801-876B-3	Sequence 3, Appli
	15	19	1.1	148567	14	US-10-254-869-3	Sequence 3, Appli
	16	19	1.1	9025608	14	4 US-10-156-761-1	Sequence 1, Appli
С	17	19	1.1	9025608	14	4 US-10-156-761-1	Sequence 1, Appli
	18	18	1.1	25	14	US-10-098-263B-74396	Sequence 74396, A
	19	18	1.1	30	9	US-09-938-641-3	Sequence 3, Appli
	20	18	1.1	201	10	US-09-878-574-3044	Sequence 3044, Ap
С	21	18	1.1	289	14	US-10-043-487-210	Sequence 210, App
С	22	18	1.1	445	11	US-09-918-995-31696	Sequence 31696, A
	23	18	1.1	. 491	10	US-09-867-701-10816	Sequence 10816, A
	24	18	1.1	598	13	US-10-027-632-193306	Sequence 193306,
	25	18	1.1	598	13	US-10-027-632-193307	Sequence 193307,
	26	18	1.1	598	13	US-10-027-632-193308	Sequence 193308,
	27	18	1.1	603	13	US-10-027-632-277321	Sequence 277321,
С	28	18	1.1	656	13	US-10-027-632-104782	Sequence 104782,
	29	18	1.1	715	13	US-10-027-632-11980	Sequence 11980, A
	30	. 18	1.1	723	10	US-09-938-842A-1654	Sequence 1654, Ap
	31	18	1.1	754	13	US-10-027-632-152169	Sequence 152169,
С	32	18	1.1	875	13	US-10-027-632-145072	Sequence 145072,
С	33	18	1.1	875	13	US-10-027-632-145073	Sequence 145073,
С	34	18	1.1	922	14	US-10-106-698-1948	Sequence 1948, Ap
С	35	18	1.1	2049	13	US-10-027-632-97200	Sequence 97200, A
С	36	18	1.1	2049	13	US-10-027-632-100266	Sequence 100266,
С	37	18	1.1	2049	13	US-10-027-632-100267	Sequence 100267,
	38	18	1.1	2344	13	US-10-044-090-745	Sequence 745, App
	39	18	1.1	3091	11	US-09-983-000A-1	Sequence 1, Appli
	40	1.8	1.1	3828	14	US-10-156-761-2959	Sequence 2959, Ap
С	41	18	1.1	4465	10	US-09-964-824A-267	Sequence 267, App
С	42	18	1.1	4465	11	US-09-984-842-1	Sequence 1, Appli
	43	18	1.1	7941	10	US-09-954-456-1812	Sequence 1812, Ap
	44	18	1.1	7941	11	US-09-983-000A-5	Sequence 5, Appli
	45	18	1.1	8058	11	US-09-983-000A-3	Sequence 3, Appli

ALIGNMENTS

OM nucleic - nucleic search, using sw model

Run on: August 12, 2003, 13:19:53; Search time 3283 Seconds

(without alignments)

12400.243 Million cell updates/sec

Title: US-09-938-641-1

Perfect score: 1675

Sequence: 1 gccaaccgcagggcatttac.....ttactggcagcacgatgatc 1675

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size : 0

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*

1: em estba:*

'2: em esthum:*

3: em_estin:*

4: em estmu:*

5: em estov:*

6: em estpl:*

7: em estro:*

8: em htc:*

gb est1:* 9:

10: gb_est2:*

11: gb htc:*

12: gb est3:*

13: gb est4:*

14: gb_est5:*

15: em estfun:*

16: em_estom:* 17: em gss hum:*

18: em gss inv:*

19: em_gss_pln:* 20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em gss pro:*

25: em_gss_rod:*

26: em gss phg:*

27: em_gss_vrl:*

28: gb_gss1:* 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

D			8				
Res		0	Query	T	D.D.	T.D.	
	No.	Score	Match	Length	DB	ID	Description
C	1	21	1.3	621	13	BU547356	BU547356 GM880013A
c	2	20	1.2	65	9	AA106910	AA106910 ml85b05.r
С	3	20	1.2	134	10	BE234275	BE234275 141082 MA
c	4	20	1.2	171	10	BE234273	BE234273 141082 MA BE234087 140686 MA
C	5	20	1.2	207	10	BE234007	BE234007 140000 MA BF703787 MI-P-E4-a
	6	20	1.2	229	10	BF703707	
	7	20	1.2	230	13	BQ598937	BF703194 MI-P-E4-a
С	8	20	1.2	234	9	AW619198	BQ598937 MI-P-E4-a
C	9	20	1.2	234	13		AW619198 540 MARC
	10	20				BQ599092	BQ599092 MI-P-E4-a
	11		1.2	324	10	BF703696	BF703696 MI-P-E4-a
_		20	1.2	329	13	BQ599184	BQ599184 MI-P-E4-a
С	12	20	1.2	334	13	BY118299	BY118299 BY118299
	13	20	1.2	337	10	BF712465	BF712465 MI-P-E4-a
	14	20	1.2	338	10	BF703795	BF703795 MI-P-E4-a
	15	20	1.2	339	10	BF703649	BF703649 MI-P-E4-a
С	16	20	1.2	340	13	BY074579	BY074579 BY074579
С	17	20	1.2	345	13	BY038194	BY038194 BY038194
С	18	20	1.2	346	10	BF321002	BF321002 uz58b12.y
	19	20	1.2	350	13	BQ598958	BQ598958 MI-P-E4-a
С	20	20	1.2	353	9	AA110753	AA110753 mm01e05.r
С	21	20	1.2	354	13	BY186446	BY186446 BY186446
С	22	20	1.2	356	13	BY043325	BY043325 BY043325
С	23	20	1.2	357	10	BB870151	BB870151 BB870151
	24	20	1.2	357	13	BQ598946	BQ598946 MI-P-E4-a
С	25	20	1.2	361	14	CB600576	CB600576 AGENCOURT
С	26	20	1.2	365	13	BY082798	BY082798 BY082798
С	27	20	1.2	366	13	BY046045	BY046045 BY046045
C	28	20	1.2	367	13	BY060917	BY060917 BY060917
	29	20	1.2	372	10	BF703685	BF703685 MI-P-E4-a
С	30	20	1.2	373	13	BY050330	BY050330 BY050330
	31	20	1.2	374	10	BF703655	BF703655 MI-P-E4-a
С	32	20	1.2	377	13	BY055356	BY055356 BY055356
	33	20	1.2	380	13	BQ599370	BQ599370 MI-P-E4-a
C	34	20	1.2	381	13	BY297534	BY297534 BY297534
С	35	20	1.2	382	13	BY039115	BY039115 BY039115
	36	20	1.2	383	13	BQ598982	BQ598982 MI-P-E4-a
	37	20	1.2	384	10	BF712107	BF712107 MI-P-E4-a
С	38	20	1.2	385	13	BY035249	BY035249 BY035249
	39	20	1.2	390	13	BQ599035	BQ599035 MI-P-E4-a
	40	20	1.2	393	9	AV834076	AV834076 AV834076
С	41	20	1.2	393	28	BH342756	BH342756 CH230-890
	42	20	1.2	398	13	BQ599018	BQ599018 MI-P-E4-a
С	43	20	1.2	398	14	CB707657	CB707657 AMGNNUC:N
С	44	20	1.2	401	12	BJ267400	BJ267400 BJ267400
	45	20	1.2	401	13	BY600926	BY600926 BY600926
•				.01		21000720	D1000920 D1000920

OM nucleic - nucleic search, using sw model

Run on: August 12, 2003, 13:24:18; Search time 124 Seconds

(without alignments)

5962.232 Million cell updates/sec

Title: US-09-938-641-1

Perfect score: 1675

Sequence: 1 gccaaccgcagggcatttac.....ttactggcagcacgatgatc 1675

Scoring table: OLIGO_NUC Gapon 60.0, Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2 6/ptodata/1/ina/6A COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ult No.	Score	% Query Match	Length	DB	ID	Description
	1	1.0	1 1	2006			
	Т	19	1.1	3926	2	US-08-731-722-1	Sequence 1, Appli
C	2	19	1.1	3926	2	US-08-731-722-1	Sequence 1, Appli
	3	19	1.1	3926	2	US-08-731-722-2	Sequence 2, Appli
С	4	19	1.1	3926	2	US-08-731-722-2	Sequence 2, Appli
	5	19	1.1	3933	2	US-08-731-722-3	Sequence 3, Appli
С	6	19	1.1	3933	2	US-08-731-722-3	Sequence 3, Appli
	7	19	1.1	148567	4	US-09-801-876B-3	Sequence 3, Appli
С	8	18	1.1	423	4	US-09-641-638-566	Sequence 566, App
С	9	18	1.1	423	4	US-09-641-638-567	Sequence 567, App
С	10	18	1.1	423	4	US-09-641-638-568	Sequence 568, App
С	11	18	1.1	423	4	US-09-641-638-569	Sequence 569, App